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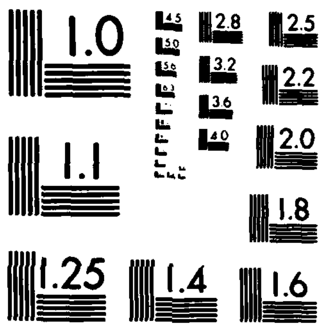

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REGENERATIVE STRUCTURE OF MARKOV CHAINS SIMULATED VIA COMMON RANDOM NUMBERS

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ABSTRACT

A standard strategy in simulation, for comparing two stochastic systems, is to use a common sequence of random numbers to drive both systems. Certain theoretical and methodological results require that the coupled system be regenerative. It is shown that if the stochastic systems are Markov chains with countable state space, then the coupled system is necessarily regenerative. An example is given which shows that the regenerative property can fail to hold in general state space, even if the individual systems are regenerative.

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SIGNIFICANCE AND EXPLANATION

Suppose that a simulator wishes to compare the steady-state performance of two stochastic systems. A natural way to do this is to subject each of the systems to the same sequence of random disturbances. In other words, one drives each system with the same random inputs. This is known, in the simulation literature, as the method of common random numbers. One of the most powerful tools available for analyzing steady-state simulation problems requires that the process being simulated be regenerative. Roughly speaking, this means that the process, when viewed on an appropriate random time scale, behaves like a sequence of independent and identically distributed random variables. In this paper, we relate the above concepts by obtaining conditions under which a process simulated via common random numbers is regenerative.

The responsibility for the wording and views expressed in this descriptive summary lies with MRC, and not with the author of this report.

REGENERATIVE STRUCTURE OF MARKOV CHAINS SIMULATED VIA COMMON RANDOM NUMBERS

Peter W. Glynn

1. Introduction

For $i = 1,\ldots,m$, let $X_i = \{X_i(n) : n \geq 0\}$ be a Markov chain on state space E_i. Assuming that the X_i's correspond to m alternative designs for a new system, one would like to compare the m designs. To be precise, one would like to determine the chain X_r which minimizes $r_i = Ef_i(X_i)$ over $1 \leq i \leq m$, where the $f_i(X_i)$'s are real-valued cost functionals. Simulators, when faced with this problem, frequently use the method of common random numbers. In other words, rather than simulating the m chains independently, one drives all m chains using the same sequence of random inputs. Since each chain is subjected to the same random disturbances, one hopes that the statistical efficiency of the comparison procedure will be improved, through a variance reduction of some sort.

HEIDELBERGER and IGLEHART (1979) studied this problem, in the case that the $f_i(X_i)$'s take the form

$$f_i(X_i) = \lim_{n\to\infty} \frac{1}{n} \sum_{k=0}^{n-1} g_i(X_i(k)) \quad ,$$

for some function $g_i : E_i \to \mathbb{R}$. They showed that when $m = 2$, efficiency of the simulation experiment is indeed improved when the X_i's and g_i's are suitably monotone. Their argument required that the paired process (X_1,X_2) be a positive recurrent regenerative sequence; no verifiable conditions guaranteeing this regenerative property were given, however. In this note, we shall show that if $E_1,\ldots,E_m$ are countable and if the X_i's are positive recurrent chains, then the joint process $(X_1,\ldots,X_m)$ is regenerative. We conclude with an example which shows that the result can fail if the E_i's are uncountable.

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2. The Main Result

Our main result will require that the E_i's be countable. Thus, without loss of generality, we may assume that $E_i \subseteq Z^+ = \{0,1,\ldots\}$ for $1 \le i \le m$. Let $P_i = (p_i(j,k) : j,k \in E_i)$ be the transition matrix for the Markov chain X_i, and let $\mu_i = (\mu_i(j) : j \in E_i)$ be the associated initial distribution. A Markovian coupling of the processes $X_1,\ldots,X_m$ is a Markov chain $X = \{X(n) : n \ge 0\}$ satisfying:

(2.1) i.) for $n \ge 0$, $X(n) \equiv (X(1,n),\ldots,X(m,n)) \in E \equiv E_1 \times\ldots\times E_m$,

ii.) for $1 \le i \le m$, $P\{X(i,0) = j\} = \mu_i(j)$, $j \in E_i$,

iii.) for $1 \le i \le m$, $n \ge 0$,

$$P\{X(i,n+1) = k \mid X(i,n) = j\} = p_i(j,k),\ j,k \in E_i.$$

The method of common random numbers, as practiced in simulation, leads naturally to Markovian couplings.

(2.2) Example. In general, Markov chains are simulated through recursions of the form

$$X_i(k+1) = h_i(X_i(k),\ \xi_i(k+1))$$

where $\xi_i = \{\xi_i(k) : k \ge 1\}$ is a sequence of independent and identically distributed (i.i.d.) random variables (r.v.'s). For example, if the process is generated through inversion, then the $\xi_i(k)$'s are uniform on $[0,1]$; see p. 807 of [4] for details. In any case, if the ξ_i's, $1 \le i \le m$, have a common distribution, as occurs through inversion, one can use the stream of random numbers ξ_1 to generate all m chains via the recursions $X(i,k+1) = h_i(X(i,k),\ \xi_1(k+1))$; this Markovian coupling is the method of common random numbers.

(2.3) Example. Suppose that $P_1 = P_2$ is an irreducible positive recurrent transition matrix with invariant probability π. If $\mu_1(j) = \pi(j)$ and μ_2 is arbitrary, one is interested in studying, for a given Markovian coupling, various properties of the random time $T(D) = \inf\{n \ge 0 : X(n) \in D\}$, where D is the "diagonal" set $\{(x,y) \in E_1 \times E_2 : x = y\}$. The "coupling time" $T(D)$ provides information on the rate at which $X_2(n)$

converges to the invariant probability π; see PITMAN (1974), for example. The most frequently used coupling, in this area of study, is the <u>independent</u> coupling, in which

$$P\{X(n) = (k,\ell) \mid X(n-1) = (i,j)\} = p_1(i,k)p_2(j,\ell)$$

$$P\{X(0) = (k,\ell)\} \qquad = \pi(k)\mu(\ell)$$

for $i, j, k, \ell \in E_1$.

Let $P = (p(x,y) : x, y \in E)$ be the transition matrix of X and μ the initial distribution of X. The state space E may be partitioned into subsets $T, C_1, C_2, \ldots$ where T consists of transient states and the C_i's are irreducible closed sets of recurrent states; see ÇINLAR (1975), p. 125 - 131 for details.

(2.4) <u>Theorem</u>. Suppose $P_1,\ldots,P_m$ are irreducible positive recurrent transition matrices, with invariant probability distributions $\pi_1,\ldots,\pi_m$. Then,

i.) $C = \bigcup_{i=1}^{\infty} C_i \neq \emptyset$ consists of positive recurrent states,

ii.) $P\{T(C) < \infty\} = 1$, where $T(C) = \inf\{n \geq 0 : X(n) \in C\}$,

iii.) for $j \geq 1$, the invariant probability distribution $\pi(j;\cdot)$ concentrated on C_j satisfies

$$\pi(j;E_1 \times\ldots\times E_{i-1} \times \{k\} \times E_{i+1} \times\ldots\times E_m) = \pi_i(k),\ k \in E_i,\ 1 \leq i \leq m.$$

This theorem shows that for any Markovian coupling of countable state Markov chains, the joint process X is eventually absorbed into some closed irreducible subset C_j upon which the chain is positive recurrent. Furthermore, regardless of the class C_j into which the chain X is absorbed, the marginal distributions of the invariant probability associated with C_j will be precisely those of the original chains $X_1,\ldots,X_m$.

<u>Proof of the theorem</u>. Let X have an arbitrary initial distribution μ, and consider the probability measures defined by

$$Q_n(\cdot) = \frac{1}{n}\sum_{k=0}^{n-1} P\{X(k) \in \cdot\}$$

$$Q_n(i,\cdot) = \frac{1}{n}\sum_{k=0}^{n-1} P\{X(i,k) \in \cdot\} \quad .$$

Since X_i has invariant probability π_i by assumption, standard Markov chain theory, plus (2.1) iii.), shows that $Q_n(i,\cdot) \Longrightarrow \pi_i(\cdot)$ in the discrete topology on E_i (see p. 16 of BILLINGSLEY (1968)), where $\Longrightarrow$ denotes weak convergence. Thus, $\{Q_n(i,\cdot) : n \geq 1\}$ is tight (see Theorem 6.2 of [2]) i.e., for any $\varepsilon > 0$, there exists a compact set $K_i = K_i(\varepsilon)$ (consisting of finitely many points) such that $Q_n(i,K_i(\varepsilon)) > 1 - \varepsilon/m$. Set $K = K_1 \times \ldots \times K_n$ and observe that $K = \bigcap_{i=1}^{m} E_1 \times \ldots \times E_{i-1} \times K_i \times E_{i+1} \times \ldots \times E_n$. Thus, for any $n \geq 1$,

$$\begin{aligned} Q_n(K) = 1 - Q_n(K^c) &= 1 - Q_n\Big(\bigcup_{i=1}^{m} E_1 \times \ldots \times E_{i-1} \times K_i^c \times E_{i+1} \times \ldots \times E_m\Big) \\ &\geq 1 - \sum_{i=1}^{m} Q_n(E_1 \times \ldots \times E_{i-1} \times K_i^c \times E_{i+1} \times \ldots \times E_m) \\ &= 1 - \sum_{i=1}^{m} Q_n(i,K_i^c) > 1 - \varepsilon \quad . \end{aligned}$$

Since K has finitely many points, and is therefore compact in the discrete topology, it follows that $\{Q_n(\cdot) : n \geq 1\}$ is tight. Thus, by Theorem 6.1 of [2], we are guaranteed the existence of a subsequence n_k and a probability $\pi(\cdot)$ such that

$$Q_{n_k}(\cdot) = \frac{1}{n_k}\sum_{j=0}^{n_k-1} P\{X(j) \in \cdot\} \Longrightarrow \pi(\cdot)$$

as $k \to \infty$. Select $x \in E$ so that $\pi(\{x\}) > 0$. Since $Q_{n_k}(\{y\}) \to 0$ for transient or null recurrent states y, it must be that x is positive recurrent, so that $C \neq \emptyset$. Furthermore, by concentrating μ on C_j, it follows that C_j contains a positive recurrent state, so that evidently C_j must have all states positive recurrent (see Theorem 3.16 of [3]).

For (2.4) ii.), note that

$$P\{T_C < \infty\} \geq \overline{\lim_{k\to\infty}} \frac{1}{n_k} \sum_{j=0}^{n_k-1} P\{X(j) \in C\}$$

$$= \sum_{x\in C} \pi(\{x\}) = 1 \quad ,$$

since our discussion above shows that π must be concentrated on positive recurrent states. For the last assertion, let μ be the invariant probability $\pi(j;\cdot)$ concentrated on C_j and observe that

$$\pi(j;E_1 \times\ldots\times E_{i-1} \times \{k\} \times E_i \times\ldots\times E_n)$$

$$= Q_n(E_1 \times\ldots\times E_{i-1} \times \{k\} \times E_i \times\ldots\times E_n)$$

$$= Q_n(i,\{k\}) \to \pi_i(k) \quad ;$$

the first equality is by invariance of $\pi(j;\cdot)$, and the convergence follows from (2.1) iii.).

(2.3) <u>Example</u> (continued). Suppose that $P_1 = P_2$ is an aperiodic irreducible positive transition matrix. Then, under the independent coupling, the state space E of X is easily seen to be irreducible. By Theorem 2.4, it follows that X has one positive recurrent irreducible class of states C.

A natural question to ask at this point is whether the set of transient states T can be non-empty. The following example shows that this is in fact possible.

(2.5) <u>Example</u>. Let $m = 2$ in Example 2.2, and suppose that $h_i : Z^+ \times [0,1] \to Z^+$ satisfies:

i.) $P\{h_1(i,U) = 1\} = 0 \quad , \quad i \neq 0$

ii.) $P\{h_2(i,U) = 1\} = 0 \quad , \quad i \neq 2$

iii.) $h_1(0,x) = 1$ if and only if $x > 1/2$

iv.) $h_2(2,x) = 1$ if and only if $x \leq 1/2$,

where U is a uniform r.v. and the h_i's are mappings under which the X_i's are irreducible and positive recurrent. For $i = 1,2$, set $X(i,0) = 1$ and put $X(i,k+1) =$

$h_i(X_i(k),U_{k+1})$, where $\{U_k : k > 1\}$ is a sequence of i.i.d. uniform r.v.'s. We claim that for $n > 1$,

$$P\{X(n) = (1,1) \mid X(0) = (1,1)\} = 0 \quad ,$$

which clearly implies that $(1,1)$ is transient for X. Note that by (2.4) i.) - ii.), $X(n) = (1,1)$ only if $X(n-1) = (0,2)$. But

$$\begin{aligned} &P\{X(n) = (1,1) \mid X(n-1) = (0,2)\} \\ &= P\{h_1(0,U_n) = 1 = h_2(2,U_n)\} = 0 \end{aligned}$$

by (2.4) iii.) - iv.).

This has implications for the regenerative method of simulation (see IGLEHART (1978) for details), as applied to steady state analysis of countable state Markov chains generated via common random numbers. By Example 2.5, the simulation may start in a transient state if the initial distribution of X is not chosen carefully. However, Theorem 2.4 shows that X is eventually absorbed into a closed positive recurrent irreducible class C_j. Once X is in C_j, the standard regenerative method may be applied, using any state in C_j as "regeneration state." The difficulty, of course, is determining precisely when X has entered an absorbing recurrent class.

3. A Nonregenerative Markovian Coupling

We will produce a nonregenerative process $X = (X(1,\cdot), X(2,\cdot))$, in which X is obtained from regenerative component processes via the method of common random numbers. To be precise, we shall choose $X(1,\cdot)$ and $X(2,\cdot)$ to be Markov chains, having identical transition functions, which are individually positive recurrent regenerative sequences (positive recurrence shall mean here that the expected time between regenerations is finite), for any initial condition. However, we will show that if $X(1,0) \neq X(2,0)$, the joint chain X is not a positive recurrent regenerative sequence.

Let $E = \mathbb{R}$ and put $h(x,y) = (\frac{1}{2}x) + y$. Assume that $P\{\xi(k+1) \in dx\} = f(x)dx$, $i = 1,2$, where:

i.) f is continuous and positive on $\mathbb{R}$

ii.) $\alpha = E|\xi(k+1)| < \infty$.

The concept of a Markovian coupling generalizes, in the obvious way, to Markov chains taking values in $\mathbb{R}$.

(3.1) <u>Proposition</u>. The Markov chain Z defined by $Z(k+1) = h(Z(k), \xi(k+1))$ is a positive recurrent regenerative sequence.

<u>Proof</u>. We will prove that there exists a set A, a positive number λ, and a probability measure ϕ on E such that:

a.) $P\{T(A) < \infty \mid Z(0) = z\} = 1$ for all

$z \in E$, where $T(A) = \inf\{n \geq 1 : Z(n) \in A\}$.

b.) $P\{Z(1) \in \cdot \mid Z(0) = z\} \geq \lambda\phi(\cdot)$

for all $z \in A$.

Conditions a.) and b.) allow one to use a "splitting technique" due to ATHREYA and NEY (1978) and NUMMELIN (1978) to construct regeneration times for Z, under any initial condition.

Let $A = \{z : |z| \leq 2(\alpha+1)\}$; we use a "test function" criterion due to TWEEDIE (1976) to verify a.). Note that for $z \notin A$, and $k(\cdot) = |\cdot|$,

$$E\{k(Z(1)) \mid Z(0) = z\} = E|(\tfrac{1}{2})z + \xi(1)|$$

$$\leq (\tfrac{1}{2})|z| + \alpha \leq 2\alpha + 1 \leq k(z) - 1$$

from which it follows (see Theorem 6.1 of [9]) that $E\{T(A) \mid Z(0) = z\} \le k(z) < \infty$ for $z \notin A$, proving a.).

For b.), let $\lambda = 2 \min\{f(z) : |z| \le \alpha+2\}$, $s(y) = 1/2$ on $[-1,1]$ and zero elsewhere, and observe that

$$\begin{aligned} P\{Z(1) \in B \mid Z(0) = z\} &= P\{(1/2)z + \xi(1) \in B\} \\ &= \int_B f(y - (1/2)z)dy \ge \lambda \int_B s(y)dy \equiv \lambda\phi(B) \end{aligned}$$

for $z \in A$. For the positive recurrence, note that our above bound on the expected hitting time of A shows that

$$\begin{aligned} \sup_{z\in A} E\{T(A) \mid Z(0) = z\} &\le \sup_{z\in A} E\{k(Z(1)) \mid Z(0) = z\} + 1 \\ &\le \sup_{z\in A} |z| + \alpha + 1 < \infty \quad . \end{aligned}$$

Since A is compact with positive ϕ-measure, and the transition function of Z is weakly continuous, it follows that A is a status set for Z; the above bound then proves that Z has an invariant probability measure. (See Proposition 5.4 and Theorem 9.1 of [9] for results and definitions.) Theorem 6.1 of [1] yields the positive recurrence as a consequence.

Define $X(i,\cdot)$ via the recursion $X(i,k+1) = (1/2)X(i,k) + \xi(k+1)$. Then,

$$X(i,k) = \sum_{j=1}^{k} 2^{j-k}\xi(j) + 2^{-k}X(i,0) \quad .$$

Clearly, $X(n)$ converges weakly to $Y = (Y_1,Y_2)$ where $Y_1 = Y_2$ a.s. Suppose that X is a positive recurrent regenerative sequence with regeneration times $T_1, T_2, \ldots$. Then,

$$\frac{1}{n}\sum_{k=0}^{n-1} P\{X(k) \in B\} \to \frac{E\{\sum_{k=T_1}^{T_2-1} I(X(k) \in B)\}}{E\{T_2 - T_1\}} \equiv \pi(B)$$

by SMITH (1954), p. 27. It is easily verified that the set function $\pi(\cdot)$ must be a probability measure, and thus $\pi(\cdot) = P\{Y \in \cdot\}$. Hence, setting $B = \{(x_1,x_2): x_1 = x_2\}$ in (3.2) yields

$$0 = \frac{1}{n} \sum_{k=0}^{n-1} P\{X(1,k) = X(2,k)\} \neq P\{Y_1 = Y_2\} = 1 \quad ,$$

if $X(1,0) \neq X(2,0)$. This contradiction shows that X is not a positive recurrent regenerative sequence.

References:

1. ATHREYA, K. B. and NEY, P. (1978). A new approach to the limit theory of recurrent Markov chains. Trans. Amer. Math. Soc. 245, 493-501.
2. BILLINGSLEY, P. (1968). Convergence of Probability Measures. Wiley, New York.
3. ÇINLAR, E. (1975). Introduction to Stochastic Processes. Prentice-Hall, Englewood Cliffs, NJ.
4. HEIDELBERGER, P. and IGLEHART, D. L. (1979). Comparing stochastic systems using regenerative simulation with common random numbers. Advances in Appl. Probability 11, 804-819.
5. IGLEHART, D. L. (1978). The regenerative method for simulation analysis. In Current Trends in Programming Methodology, III. Software Modeling. ed. K. M. Chandy and R. T. Yeh, Chapter 2, 52-71, Prentice-Hall, Englewood Cliffs, NJ.
6. NUMMELIN, E. (1978). A splitting technique for Harris recurrent Markov chains. Z. Wahrscheinlichkeitstheori8 und verw. Gebiete 43, 309-318.
7. PITMAN, J. W. (1974). Uniform rates of convergence for Markov chain transition probabilities. Z. Wahrscheinlichkeitstheori8 verw. Gebiete 29, 193-227.
8. SMITH, W. L. (1955). Regenerative stochastic processes. Proc. R. Soc. London A 232, 6-31.
9. TWEEDIE, R. L. (1976). Criteria for classifying general Markov chains. Advances in Appl. Probability 8, 737-771.

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